<u>REMARKS</u>

The present application was filed on February 20, 2004 with claims 1-19. Claims 4-7, 10-12, 15, 16, 18, and 19 have been withdrawn. Claims 1, 8, 13, and 17 are the pending independent claims.

In the final Office Action dated July 10, 2008, the Examiner: (i) rejected claim 17 under 35 U.S.C. §112, second paragraph; and (ii) rejected claims 1-3, 8, 9, 13, 14, and 17 under 35 U.S.C. §102(b) as being anticipated by U.S. Patent No. 5,706,498 to Fujimiya et al. (hereinafter "Fujimiya").

With regard to the §112 rejection of claim 17, Applicant respectfully amends claim 17 by removing the phrase "that may be bound to a target nucleotide sequence." This amendment is consistent with the amendments made to independent claims 1, 8, and 13 in Applicant's previous response dated March 28, 2008. Accordingly, Applicant respectfully requests withdrawal of the §112 rejection of claim 17.

With regard to the §102 rejection of claims 1-3, 8, 9, 13, 14, and 17, Applicant initially notes that MPEP §2131 specifies that a given claim is anticipated "only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference," citing <u>Verdegaal Bros. v. Union Oil Co. of California</u>, 814 F.2d 628, 631, 2 U.S.P.Q.2d 1051, 1053 (Fed. Cir. 1987). Moreover, MPEP §2131 indicates that the cited reference must show the "identical invention . . . in as complete detail as is contained in the . . . claim," citing <u>Richardson v. Suzuki Motor Co.</u>, 868 F.2d 1226, 1236, 9 USPQ2d 1913, 1920 (Fed. Cir. 1989).

As argued in Applicant's previous responses, Applicant asserts that Fujimiya fails to anticipate each and every limitation of the recited claims. Applicant notes that Fujimiya teaches a gene database retrieval system where a key sequence is compared to database sequences. The way in which Fujimiya carries out his comparison is very distinct. Fujimiya uses a scoring system to find the most agreeable combination of the target data and the key data. See Fujimiya, FIGS. 7a and 7b; and Fujimiya, col. 3, ll. 32-65. Specifically, Fujimiya determines an "optimal disposition" using score values of lattice points of a matrix. Fujimiya connects the highest scored lattice points of the matrix to determine the optimal disposition. Fujimiya, col. 3, ll. 53-

65. Applicant submits that Fujimiya's disclosure focuses on obtaining the "maximal sum values" (i.e., the best matching target data). Fujimiya, col. 9, ll. 20-45.

Applicant believes that Fujimiya fails to anticipate the recited claims. For instance, Fujimiya does not teach evaluating a binding possibility as recited in the claims. The claims recite performing the evaluation in accordance with an edit distance. An edit distance is the number of times nucleotides of a subsequence are required to be adjusted to generate complementary sequence data. <u>See</u> Claim 1. An exemplary embodiment of edit distance is described in the specification at, for example, page 14, lines 1-10 with reference to figure 1(b). Fujimiya does not disclose an edit distance as recited in the claims and supported in the specification. Applicant notes that Fujimiya does disclose a system of scoring that is related to insertions, deletions, and substitutions; however, Fujimiya's system of scoring (e.g., adding and subtracting points) does not anticipate the recited edit distance.

Further, as argued in Applicant's previous response, the claims recite that the evaluation result of the evaluation process is used by a user in <u>determining binding effectiveness and reliability of the probe nucleotide sequence to the target nucleotide sequence</u>. Applicant believes that this language, at the very least, distinguishes the recited claims from Fujimiya. Fujimiya is not concerned with determining binding effectiveness and reliability of a probe nucleotide sequence. Fujimiya simply retrieves genes from a gene database using a sequence as a key.

Notwithstanding the above arguments, Applicant respectfully amends the recited claims without prejudice and solely to expedite prosecution of the present application. Specifically, Applicant clarifies the recited limitation of "descending order of edit distance." Independent claim 1 now recites, "wherein the evaluation is performed in descending order from a first edit distance value to a second edit distance value, the second edit distance value being lower than the first edit distance value, further wherein an edit distance is the number of times nucleotides of the subsequence are required to be adjusted to generate the complementary sequence data." Further, Applicant amends independent claims 8, 13, and 17 to recite subject matter similar to claim 1. For example, independent claim 8 now recites that the evaluation is performed in descending order from the maximum acceptable edit distance to a second edit distance, a value of the second edit distance being lower than a value of the maximum acceptable edit distance.

Support for these amendments may be found in the specification at, for example, p. 4, ll. 17-25 ("By way of example, in the present invention, the user designates the maximum edit distance, starts evaluation from an evaluation of whether or not only the maximum edit distance is different, and then evaluates the binding between the probe P and the target nucleotide sequence T in descending order") (emphasis added). In addition to the above amendments, Applicant has removed the phrase, "of binding precision," to avoid any possible ambiguity in the claim language.

Applicant asserts that the above clarifying amendments clearly distinguish the claims from Fujimiya. Applicant submits that Fujimiya does not disclose "descending order" as recited in the claims. The amended claims clearly recite how the claimed evaluation is performed (e.g., highest edit distance first). In response to the Examiner's arguments in the final Office Action, Applicant initially notes that the recited claim language can not be reasonably interpreted to be the processing flow of the dynamic programming for computing the degree of similarity as disclosed in FIGS. 7a and 7b of Fujimiya. See Final Office Action, p. 9, first partial paragraph. The fact that FIGS. 7a and 7b show arrows pointing downward does not anticipate, for example, claim 8 which recites that an evaluation is performed in descending order from the maximum acceptable edit distance to a second edit distance, a value of the second edit distance being lower than a value of the maximum acceptable edit distance. Even if the Examiner believes that the scoring system disclosed in Fujimiya is equivalent to the recited edit distance, Fujimiya is not performing an evaluation in descending order from a maximum acceptable edit distance (e.g., worst match first to a better match).

In fact, the Examiner concedes that Fujimiya goes from a "minimum to maximum number of operations" (e.g., best match first). Final Office Action, p. 9, first partial paragraph. Specifically, the Examiner states at p. 9, first partial paragraph of the final Office Action (emphasis added):

> As described in Fujimiya et al. (col. 2, last paragraph), one starts small, adds on, which can increase changes (i.e. number of operations). As described in Fujimiya et al. (col. 9, lines 21-67), target data is altered one after another to determine similarity to the key data and acquiring the sum data at each target data occurring
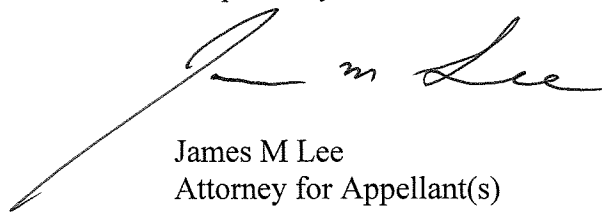
at the operation. <u>This goes from minimum to maximum number of operations</u> (i.e. descending order of edit distance).

In view of the Examiner's interpretation of Fujimiya as "best to worst," Fujimiya is in direct contrast with the recited claims. For instance, amended claim 1 recites that the evaluation is performed in descending order, specifically, from a first edit distance value to a second edit distance value, the second edit distance value being lower than the first edit distance value (e.g., the edit distance value goes down in value; worst match first).

For at least these reasons, Fujimiya fails to anticipate independent claims 1, 8, 13, and 17. It follows that dependent claims 2, 3, 9, and 14 are patentable at least by virtue of their dependency from independent claims 1, 8, and 13. Accordingly, withdrawal of the §102(b) rejection of claims 1-3, 8, 9, 13, 14, and 17 is respectfully requested.

In view of the above amendments and remarks, Applicant believes that the pending claims are in condition for allowance, and respectfully requests withdrawal of the §112 and §102(b) rejections.

Respectfully submitted,

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